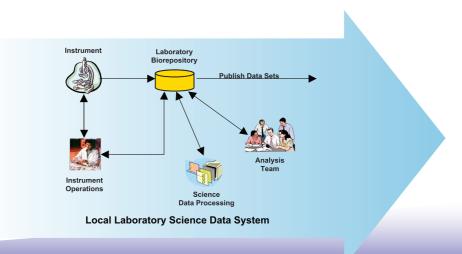
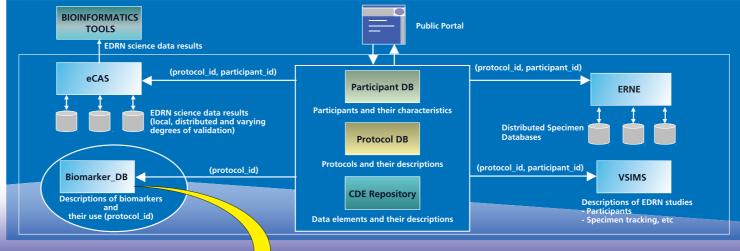
EDRN Knowledge Environment





											<u> </u>									
	POTENTIALLY USEFUL BIOMARKERS	EXPLORATORY STUDY	BIOLOGICAL MATERIALS	AFFYMETRIX GENE EXPRESSION	MICROARRAYS	GEL PROCESSING	PROTEIN ASSAYS	MASS SPECTROMETRY	PROTEIN IDENTIFICATION	DATA ANALYSIS	RESULTS	FINDINGS	REFERENCE	TISSUE PREPARATION PROTOCOL	SLIDE PREPARATION PROTOCOL	MICRODISSECTION PROTOCOL	PROCESSING OF MICRODISSECTED TISSU	E DNA ANALYSIS PROTOCOL	RNA ANALYSIS PROTOCOL	PROTEIN ANALYSIS PROTOCOL
	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)		Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)	PROTOCOL	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)
	Superiums	1 4 1	1 4. /	1	1 4, ,		1 47 /	1 0, ,		Name of the biomarker (e.g., CC2)			Cancer type (e.g., colon cancer)	1			Name of the biomarker (e.g., CC2)	Cancer type (e.g., colon cancer)	Cancer type (e.g., colon cancer)	Cancer type (e.g., colon cancer)
	Concerture (e.g. colon concert	Cancer type (e.g., colon cancer)	Cancer type (e.g., colon cancer)	Cancer type (e.g., colon cancer)	Cancer type (e.g., colon cancer) Description of LCM (Laser Capture	Cancer type (e.g., colon cancer)	Cancer type (e.g., colon cancer)	Cancer type (e.g., colon cancer) Description of Mass Spectrometry (MS)	Cancer type (e.g., colon cancer)	Cancer type (e.g., colon cancer)	Cancer type (e.g., colon cancer)	Cancer type (e.g., colon cancer) Technology used for measurement of	Link to ERNE reference	Cancer type (e.g., colon cancer) Tissue preparation description	Cancer type (e.g., colon cancer) Slide preparation description	Cancer type (e.g., colon cancer) Microdissection description	Cancer type (e.g., colon cancer)	DNA analysis description	RNA analysis description	Protein analysis description
	Cancer type (e.g., colon cancer) Description of the biological rationale	Specimen type (e.g., serum-based) Study type (e.g., DNA, RNA, Protein)	Type of biological material used (e.g., whole tissue, cytology sample, blood)	1 0, ,	Microdissection)	Description of gel processing experiment	Protein assay protocol	experiment experiment	Description of protein identification	Selected type of samples to compare	Case (e.g., invasive CRC)	gene/protein expression (e.g., 2-DE, LC,	Link to eCAS reference	70% Ethanol Fixation	For Laser Capture Microdissection (LCM)	Laser Capture Microdissection (LCM)	Processing description	Clonality: X-chromosome Inactivation	Gene-specific RT-PCR	2D-PAGE
	'			Number of controls (e.g., 10)	Description of microarray experiment	Image processing software name and version	, , , , , , , , , , , , , , , , , , ,	MS instrument name and version	Database search program used	Selected numbers of samples to compare	Control (e.g., normal)	ICAT)	Link to Gene Ontology reference		For Mannual Microdissection	Manual Microdissection	For DNA-based studies	Comparative Genomic Hybridization (CGH)	Targeted Differential Display	Immunoblot
	Description of the justification for the potential interest	Study objective (e.g., biomarker development		Number of Affymetrix probe-sets (e.g., 7129)		Software provider	Chemical treatment	Instrument manufacturer	Software name and version	Description of the source of normal tissue	Case mean (e.g., -0.164)	Findings from measurement of gene/protein	Taxonomy (e.g., Homo sapiens)	Low-melt Polyester Embedding			For RNA-based studies	, , ,	, , , , , , , , , , , , , , , , , , , ,	
	Description of the justification for the value	Study target (e.g. nuclear matrix proteins)	Pathology sample type (e.g., bulk tissue, intraoperative diagnosis slide, histology	Number of genes observed (e.g., 4966)	Link to raw microarray data URL	Spot detection algorithm	Chemical treatment description	Description of MALDI/SELDI-TOF-MS	Database name used for protein identificatio (e.g., MSDB)	abnormal/diseased tissue	Control mean (e.g., -0.887)	expression	Taxiu (e.g., 9000)	Paraffin Embedding	Link to protocol details	Immuno-LCM	For Protein-based studies	Dideoxy Fingerprinting	Link to protocol details	Immunohistochemistry (IHC)
	of the marker	Biomarker discovery status (e.g., ongoing,		Number of training samples (e.g., 43)	Submission date of raw microarray data	Spot matching algorithm	Description of treated analyte	Description of MALDI/SELDI-TOF-MS/M		-	Up/down (e.g., up)	Findings from measurement of protein	Link to Genecards reference	Link to protocol details	PI name		Link to protocol details	Loss of Heterozygosity	Pl name	Protein sample preparation for Mass Spectrometry
	Description of the suggestion for further	complete)	cytology specimen)	Number of genes from training samples (e.g.,	Summary of microarray experiment analysis	Link to protocol details	Description of Luminex Multianalyte Profilin (xMPA) panel assay	Description of LC-ESI-MS/MS	11.07	Description of comparative analysis Statistical method description	t-test (e.g., -4.917)	composition of organelles	Link to Aliases and descriptions (HGNC, Entrez Gene, UniProt/Swiss-Prot.	Piname	Institution	PI name Institution	PI name	Link to protocol details PI name	Institution Comments	Staining procedures
Phase 1	investigation	Approach (e.g., proteomics, glycomics,	Microdissected tumor	Link to mothe de detaile	Description of CGH (Comparative Genomic	Link to band files URL	Link to protocol details URL	Description of LC-MALDI/SELDI-MS/MS	Number of sequences at this timestamp (e.g. 1.942.918)	1	p-value (e.g., 0.0004)	Findings from analysis of post-translational	UniProt/TrEMBL, GDB, OMIM, GeneLoc)	Institution	Comments		Institution		Comments	Surface Enhanced Laser Desorption
	Evaluation of the discriminant ability in	methylation, genomics, libraries and immune		Link to methods details	Hybridization) experiment	Link to 1-D gel files URL	<u> </u>	Link to protocol details URL	Number of residues at this timestamp (e.g.,	Significance testing description	adjusted p-value (e.g., 0.0004)	modifications	Link to Genomics location (GeneLoc. HGNC.	Comments		Comments	Comments	Institution Comments	AI	Ionization (SELDI)
Preclinical	distinguishing cancer cases and controls	response, autoabs, mice models, spectral	Description of the protocol used for sample	Method of processing Affymetrix chips Method of quantile-normalizing the data	Link to raw array CGH experiment data URL	Link to 2-D gel files URL	Link to raw data files URL PI name		629,040,812)	Normalization technique	Confidence intervals	Findings from analysis of protein-protein	Entrez Gene, UCSC, Ensemble)				Continents	Comments	AI	MALDI
	Evaluation of the predictive ability of this	imaging, gene expression)	processing			Link to DIGE gel files URL		Link to MS peak list files URL	Link to protein matched list URL	Description of the biomarker examined in normal versus diseased	Results of sensitivity analyses	interactions	Link to Proteins (UnitProt/Swiss-Prot,							Link to protocol details
Exploratory	biomarker	Technology (e.g., SELDI-TOF-MS)	Link to the protocol details URL	Method of creating annotation for the probe- sets on the chips	data	Summary of gel processing experiment analysis results	Institution	Statistical method description	Link to peptide matched list URL	Description of the biomarker examined in	Results of specificity analyses	Findings from analysis of protein-drug	RefSeq, Ensemble)							PI name
	Sensitivity %	Description of pre-specified hypotheses	Cancer status from which the specimen was		Summary of CHG experiment analysis results	Di nome	Comments	Type of statistical method (e.g., parametric, semi-parametric, non-parametric)	Top scored hit (e.g. Q9BZX6_Human)	different organ sites	Figure type (e.g., HuFL affymetrix chip, cDNA	Interactions	Link to Protein domains/families (InterPro, ProtoNet, UniProt/Swiss-Prot, Blocks)						/II	Institution
	Specificity %	PI name	collected	normal samples	Description of IHC (Immunohistochemistry)	Pi name		Type of statistical approach (e.g., model-	Significance threshold (e.g., p<0.05)	Description of the biomarker examined in	microarrays, etc.)	PI name	Link to Ontologies and pathways (Gene							Comments
Front a make may	Positive Predictive Value	Institution	Sample treatment description	Link to Intensity values for each sample for	experiment	Comments		driven, supervised, unsupervised)	Pl nama	benign diseases of the same organ	Sensitivity %	Institution	Ontology, KEGG)							Comments
Exploratory	PI name	Comments	Sample treatment type	each probe-set (gene)	Description of IHC tissue arrays	Comments		Background removal technique	Institution	Description of the biomarker examined in	Specificity % Positive Predictive Value	Comments	Link to Drugs and compounds (Bioalma,							
studios to	Institution		Sample treatment compound	Link to data analysis file	Description of IHC interpretation			Denoising technique	Comments	premalignant lesions		4	PharmGKB)						/II	4
studies to	Comments		Separation description	PI name	Description of IHC image analysis			Calibration technique	- Comments	Link to tables URL	Institution	4	Link to Transcripts (GenBank/EMBL/DDBJ, UniGene, RefSeq, UniProt/Swiss-Prot)						/II	4
identify			Hybridization description	Institution	Link to IHC raw image analysis data			Normalization technique	-	Link to figures URL	Comments	4	Link to Expression in human tissues						/II	4
identity			Extraction description	Comments	Submission date of IHC raw image analysis data			Peak modeling technique	-	Link to raw data files URL	Comments		(GeneNote, GeneAnnot, GeneTide, UniGene.						/II	4
potentially useful			Event description	Comments	Summary of IHC scoring results			Isotope deconvolution technique	-	Link to analysis files URL	1		Expression Assays)						/II	4
			Event type	1	Description of FISH (Fluorent in situ Hybridization)			Charge deconvolution technique	-	Pl name	1		Link to Similar genes in other organisms						/II	4
biomarkers			Labeling description	1	experiment			Targeted profiling technique	-	Institution	1		(HomoloGene, euGenes, SGD, MGD)						/II	4
Diomarkers			Image file name	1	Link to raw FISH data URL			Peak classification technique	-	Comments	1		Link to Paralogs (HomoloGene) Link to SNPs/Variants (NCBI SNP database.						/II	4
			Image description	1	Submission date for raw FISH data			Other techniques used	4				Link to SNPS/Variants (NCD) SNP database,							4
			Image type	1	Summary of FISH experiment analysis results			Summary of MS experiment analysis results	+				Link to Disorders & mutations (OMIM.							4
			Link to the Image URL	1	Description of ELISA (Enzyme-linked			PI name	+				UniProt, HGMD)							4
			Pl name	1	Immunosorbent Assay) experiment			Institution	+				Link to Protein structure (PDB)							4
			Institution		Link to raw protein levels data URL			Comments	-				Link to literature reference							
			Comments		Submission date for protein levels			Comments					PubMed ID							
					Summary of ELISA experiment analysis results								PubMed URL Keywords							
					PI name								Link to Web reference							
					Institution								List of all other relevant studies							
					Comments								PI name							
													Institution							
													Comments							
	CLINICAL TRIAL BIOMARKERS	EVIDENCE	VALIDATION STUDY	ACCAY METHODS	etilny needon	CASEDATA	CONTROL DATA	CYTOGENETIC DATA	CLINICAL DATA	CELL LINE DATA	DATUOLOGY IMAGE DATA	TUMOR CENETICS	MOLECULAR TARGET	PROGNOSTIC INDICATOR	CLINICAL QUESTIONS	STATISTICAL ANALYSIS METHODS	DATA ANALYSIS RESULTS	PRESENTATION	DISCUSSION	DECEDENCE
		Name of the hismarker (c. a. CC2)		ASSAY METHODS	STUDY DESIGN	CASE DATA	CONTROL DATA			CELL LINE DATA	PATHOLOGY IMAGE DATA	TUMOR GENETICS	_							Name of the highester (a.e. CC2)
	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)
	Cancer type (e.g., colon cancer)	Cancer type (e.g., colon cancer)	Cancer type (e.g., colon cancer)	Cancer type (e.g., colon cancer)	Cancer type (e.g., colon cancer)	Cancer type (e.g., colon cancer)	Cancer type (e.g., colon cancer)	Cancer type (e.g., colon cancer)	Cancer type (e.g., colon cancer)	Cancer type (e.g., colon cancer)	Cancer type (e.g., colon cancer)	Cancer type (e.g., colon cancer)	Cancer type (e.g., colon cancer)	Cancer type (e.g., colon cancer)	Cancer type (e.g., colon cancer)	Cancer type (e.g., colon cancer)	Cancer type (e.g., colon cancer)	Cancer type (e.g., colon cancer)	Cancer type (e.g., colon cancer)	Cancer type (e.g., colon cancer)
	Description of the biological rationale	Evidence Description	Specimen type (e.g., tissue-based)	Assay method description	Study design description	Case description	Control description	Cytogenetic description	Clinical data description	Cell line description	Pathology image description	Tumor genetics description	Molecular target description	Prognostic indicator description	Clinical question description	Statistical analysis description	Data analysis result description	Presentation description	Discussion description	Link to literature reference
	Description of the justification for the potential interest	Prediction for some outcome of interest	Study objective (e.g., clinical trial and validation)	Specific assay method used	Case selection method (e.g., prospective or retrospective)	Case submitter	Control submitter	Clone/cell number (e.g., 1)	Gender (e.g., female)	Cell line name	Organ/tissue of origin (e.g., colon)	Genes involved	Gene name	Standard prognostic variables	Preliminary proposal of a clinical question for which the marker might be useful	List of all specific statistical methods used	Results of multivariable analyses showing the relation of the marker to standard	Link to Kaplan-Meier plot for the effect a tumor marker on a time-to-event outcome	Description of pre-specified hypotheses	PubMed ID
	Description of the justification for the value	Evidence data that is associated with some		Specific protocol used		Cell line	Cell line	Cell count (e.g., 9)	Age in years (e.g., 0)	Source & catalog number	Tumor classification (e.g., adenocarcinoma)	Proteins involved	Protein name	Correlation between the biomarker and	Supporting data	Description of any variable selection	prognostic variables	Link to diagram to show the relation of the	Interpretation of the results in the context of the pre-specified hypotheses	of PubMed URL
	of the marker	clinical parameter Evidence data that is prognostic	Biomarker validation status (e.g., ongoing, complete)		Stratification method (e.g., stratified by stage of disease, age)		Organism	Ploidy (e.g., 2n+/-, Near-diploid 46+/- (35-57))	Hematopoietic/Tumor (e.g., solid tumor)	Tissue type	Organ/tissue affected	Allele	Pathways Ontology/functional place/function	standard prognostic variables	11 0	procedures Description of model building issues	Results of univariate analyses showing the	- 	I I Mr	neywords
Phase 2	Description of the supportion for further	Evidence data that is prognostic	Complete)	Specific kits used	Cracifications region from which access were	Diagnosis/morphology (e.g.,	Diagnosis/morphology (e.g., benign	Cytogenetic technique used	Cancer stage	Culture medium	Diagnosis	Chromosome	Ontology/functional classification	Prediction of whether the biomarker is likely	Statistical Significance value	Description of model building issues	relation between the marker and outcome	Link to other presentation files	Interpretation of the results in the context of	LINK TO Web reference

Phase 2 Clinical Assay and Validation

Studies to determine the capacity of biomarkers to distinguish between people with cancer and those without

Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)	Name of the biomarker (e.g., CC2)
Cancer type (e.g., colon cancer)	Cancer type (e.g., colon cancer)	Cancer type (e.g., colon cancer)	Cancer type (e.g., colon cancer)	Cancer type (e.g., colon cancer)	Cancer type (e.g., colon cancer)	Cancer type (e.g., colon cancer)	Cancer type (e.g., colon cancer)	Cancer type (e.g., colon cancer)	Cancer type (e.g., colon cancer)	Cancer type (e.g., colon cancer)	Cancer type (e.g., colon cancer)	Cancer type (e.g., colon cancer)	Cancer type (e.g., colon cancer)	Cancer type (e.g., colon cancer)	Cancer type (e.g., colon cancer)	Cancer type (e.g., colon cancer)	Cancer type (e.g., colon cancer)	Cancer type (e.g., colon cancer)	Cancer type (e.g., colon cancer)
escription of the biological rationale	Evidence Description	Specimen type (e.g., tissue-based)	Assay method description	Study design description	Case description	Control description	Cytogenetic description	Clinical data description	Cell line description	Pathology image description	Tumor genetics description	Molecular target description	Prognostic indicator description	Clinical question description	Statistical analysis description	Data analysis result description	Presentation description	Discussion description	Link to literature reference
escription of the justification for the	Prediction for some outcome of interest	Study objective (e.g., clinical trial and	Specific assay method used	Case selection method (e.g., prospective or	Case submitter	Control submitter	Clone/cell number (e.g., 1)	Gender (e.g., female)	Cell line name	Organ/tissue of origin (e.g., colon)	Genes involved	Gene name	Standard prognostic variables	Preliminary proposal of a clinical question for	List of all specific statistical methods used	Results of multivariable analyses showing	Link to Kaplan-Meier plot for the effect a	Description of pre-specified hypotheses	PubMed ID
otential interest	Evidence data that is associated with some	validation)	Specific protocol used	retrospective)	Cell line	Cell line	Cell count (e.g., 9)	Age in years (e.g., 0)	Source & catalog number	Tumor classification (e.g., adenocarcinoma)	Proteins involved	Protein name	Correlation between the biomarker and	which the marker might be useful	Description of any variable selection	the relation of the marker to standard	tumor marker on a time-to-event outcome	Interpretation of the results in the context of	PubMed URL
escription of the justification for the valu	e clinical parameter	Biomarker validation status (e.g., ongoing,	Specific reagents used	Stratification method (e.g., stratified by stage	Organism	Organism	Ploidy (e.g., 2n+/-, Near-diploid 46+/- (35-57))	Hematopoietic/Tumor (e.g., solid tumor)	Tissue type	Organ/tissue affected	Allele	Pathways	standard prognostic variables	Supporting data	procedures	prognostic variables		the pre-specified hypotheses	Keywords
of the marker	Evidence data that is prognostic	complete)	Specific kits used	of disease, age)	Diagnosis/morphology (e.g.,	Diagnosis/morphology (e.g., benign	Cytogenetic technique used	Cancer stage	Culture medium	Diagnosis	Chromosome	Ontology/functional classification	Prediction of whether the biomarker is likely	Statistical significance value	Description of model building issues	Results of univariate analyses showing the	1 0	Interpretation of the results in the context of	Link to Web reference
Description of the suggestion for further	Evidence data that is diagnostic	Case (e.g., invasive CRC)	Quality control procedures	Specific time period from which cases were	adenocarcinoma)	condition)	Link to image file	Cancer status (e.g., metastatic, primary	Medium selection	Method (e.g., IHC for alpha actinin)	Description of genetic changes	Anomaly (e.g., overexpression,	to serve as an independent indicator	Type (e.g., diagnosis, prognosis, prediction	Description of how model assumptions were		Link to other presentation files	other relevant studies	List of all other relevant studies
rvestigation	Evidence data that identifies sub-populations		Reproducibility assessments	taken	Site/topography (e.g., colon)	Site/topography (e.g., colon)	PI name	diagnosis/chronic, relapse)	PI name	Antibody (e.g., CD3-delta)	Mutations/aberrations (e.g., deletion)	underexpression, mutation)			verified	Estimated hazard ratio	PI name	Discussion of limitations of the study	PI name
valuation of the discriminant ability in	of patients	Case mean (e.g., -0.164)	Quantitation methods	End of the follow-up time period	Source	Inclusion and exclusion criteria	Institution	Immunphenotype	Institution	Link to pathology image file	Organ/tissue of origin (e.g., colon)	Drugs	assay characteristics		Description of how missing data were	Estimated survival probability	Institution	Discussion of implications for future	Institution
tinguishing cancer cases and controls	Findings about disease markers - diagnosis	Control mean (e.g., -0.887)		Median follow-up time period	Treatments received	Selection method (e.g., randomized or rule-	Comments	Structurally altered chromosomes (e.g., A1,	Comments	Pl name	Tumor classification (e.g., adenocarcinoma)	Interventions	Suggestion of the biomarker that is easier to		handled	Other estimated effects	Comments	research	Comments
valuation of the predictive ability of this	Findings about disease markers - patient	Up/down (e.g., up)	Reporting methods	Description of all clinical endpoints examine	Inclusion and exclusion criteria	based)		A2)		Institution	Tumor name	Molecular profiles	measure	Description of the correlation with other	Description of how biomarker values were	Confidence intervals	_	Discussion of implications for future clinical	
umarker	profiling	t-test (e.g., -4.917)	Description of how assays were performed	List of all candidate variables initially	Selection method (e.g., randomized or rule-	PI name		Tissue (e.g., organ-derived)		Comments	Treatment type	Pl name	Description of new information about the	measures	handles in the analysis	Statistical significance	_	value	4
nsitivity %	Findings about drug targets - discovery	p-value (e.g., 0.0004)	blinded to the study endpoint	considered for inclusion in models	based)	Institution		Treatments (e.g., surgery)			Treatment agent	Institution	disease	PI name	Description of methods used for cutpoint	Results of checking assumptions		PI name	4
ecificity %	Findings about drug targets – validation	adjusted p-value (e.g., 0.0004)	Description of the robustness and	Rationale for sample size	PI name	Comments		Clinical comments			Metastasis tumor	Comments	Pl name	Institution	determination	Results of internal validation		Institution	_
sitive Predictive Value	Findings about drug targets – clinical trials	Link to raw data	reproducibility of the assay	Specific effect size	Institution			Hereditary syndrome (e.g., autosomal			Pl name	-	Institution	Comments	PI name	Results of sensitivity analyses		Comments	
name	Findings about drug targets – patient	Link to tables	Inter-laboratory reproducibility	Target power	Comments			dominant, autosomal recessive)			Institution	1	Comments		Institution	Results of specificity analyses	1		-
stitution	monitoring (before, during & after treatment)	Link to figures	Intra-laboratory reproducibility	Distributions of basic demographic				Specific hereditary disorder			Comments				Comments	Pl name	1	1	
omments	PI name	PI name	Reproducibility of PCR	characteristics(e.g., age and gender)				Patient's survival status (e.g., dead or alive)			Comments					Institution	1	1	
	Institution	Institution	Description of the scalability of the assay	Distributions of standard cancer-specific				Patient's survival time in months from								Comments	1	1	
	Comments	Comments	Pl name	prognostic variables	_			operation date to death or last follow-up										1	
			Institution	Distributions of tumor marker	_			Nodal status										1	
			Comments	PI name	_			Tumor size										1	
				Institution	_			Tumor stage										1	
			II.	Comments				Tumor differentiation	1									1	
			ll .					Tumor histological type (e.g., bronchial					ll .					1	
			ll .					derived, bronchial alveolar, clear cell,										1	
			ll .					papillary)										1	
			ll .					PI name										1	
			ll .					Institution					ll .					1	
			ll .					Comments										1	
			ll .																
			l							ll .									
			l							ll .			ll .					1	
			I										I					1	
										I			I					1	
										I			I					1	
													I					1	

Phase 3 Retrospective Longitudinal Determine how well biomarkers detect preclinical disease by testing the markers against tissues collected longitudinally from research cohorts

Phase 4 Prospective Screening Identify the extent and characteristics of disease detected by the test and determine the false referral rate

Phase 5 Cancer Control Evaluate both the role of the biomarkers for detection of cancer and the overall impact of screening on the population through large-scale screening on the population through large-scale population studies

Contacts:

Jane Oh, NASA Jet Propulsion Laboratory, Jane.C.Oh@jpl.nasa.gov
Dan Crichton, NASA Jet Propulsion Laboratory, Daniel.J.Crichton@jpl.nasa.gov
Mark Thornquist, Fred Hutchinson Cancer Research Center, mthornqu@fhcrc.org
Don Johnsey, National Cancer Institute, johnsey@mail.nih.gov